



Seq_listing_US_korrigiert141102.txt
SEQUENCE LISTING

<110> Forschungszentrum Juelich GmbH; Marina Vrlijc et al.

<120> Process for the microbial production of amino acids by
boosted activity of export carriers

<130> 1

<140> US/09/105,117 PCT/DE96/02485

<141> 1998-06-17

<160> 5

<170> PatentIn Ver. 2.0

<210> 1

<211> 2374

<212> DNA

<213> Corynebacterium glutamicum

<220> (LySE)

<221> gene

<222> CDS (1016)..(1726)

<400> 1

```
ccatttgctg aaggtgttac tctgcctggc ccaattcctg cgggcgaaga agtgaaaaac 60
cctgaacctt ttcagaagta actaaggccg caatccctcg attgctgcat caacgacggc 120
gtctgtgagt ctagctagag atctagattc caggcgccat cgttgccaat acatcggtgt 180
gtcaatgggt atctcatcga ggaggatcac ttctcctgct tttagcatgg gagcagcttg 240
ggtttcggga agaagtcccc aaccaaggcc tcggcgaatt gcctcaccaa aaccttccgc 300
cgacgggaca atggatacgc gcctgcgccc cacaggacca tcgacgcgcc cgtccaggtc 360
acgggtcttga agcacatctt tgggaccgaa gcgtaagacg ggcatcgag cccaatctag 420
tttcccatca accatgtagg catcccgcaa tgaggggggt gcaatggcca agtggcgcat 480
ggttccaagt tctactactt cacatccgcg cacgggatta gcttcacggg ttaccgctcc 540
taaaacatct ccacgccgca gcaaggataa tgtgtgctgt tcatcttcca agcgcagcgt 600
gagcgttgct ccacccaag aagctacctc gttgaacacg ggaggaaacc atgtggatag 660
cgaatctgcg ttgatggcga tggttaacgg gatttcagca aggcgtccag atagttagcg 720
tttagtttct gcttgacgca acaccattt cgcgctgct tgcacaagga cttcaccgcg 780
ttcggttgct ttggccggtt ggggtgcgca taccaacact cgaccacgt gatgctcgag 840
agctttaacg cgctgactca ccgccgagg ggaaatggaa agggctaagg aggcgccttc 900

gaagctgcct tcatcaatga ttgagagcaa agtgtccagt tgaatggggt tcatgaagct 960
atattaaacc atgtaagaa ccaatcattt tacttaagta cttccatagg tcacg atg 1018
Met
1
```

Seq_Histing_US_korrigiert141102.txt

gtg atc atg gaa atc ttc att aca ggt ctg ctt ttg ggg gcc agt ctt 1066
Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu
5 10 15

tta ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga att 1114
Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile
20 25 30

aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct gac 1162
Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp
35 40 45

gtc ttt ttg ttc atc gcc gcc acc ttg gcc gtt gat ctt ttg tcc aat 1210
Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn
50 55 60 65

gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt gcc atc gct tac 1258
Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr
70 75 80

ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac aag 1306
Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys
85 90 95

gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc gat 1354
Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp
100 105 110

gac acg cct ttg gcc ggt tgc gcg gtg gcc act gac acg cgc aac cgg 1402
Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg
115 120 125

gtg cgg gtg gag gtg agc gtc gat aag cag cgg gtt tgg gta aag ccc 1450
Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro
130 135 140 145

atg ttg atg gca atc gtg ctg acc tgg ttg aac ccg aat gcg tat ttg 1498
Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu
150 155 160

gac gcg ttt gtg ttt atc gcc gcc gtc gcc gcg caa tac gcc gac acc 1546
Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr
165 170 175

gga cgg tgg att ttc gcc gct gcc gcg ttc gcg gca agc ctg atc tgg 1594
Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp
180 185 190

ttc ccg ctg gtg ggt ttc gcc gca gca gca ttg tca cgc ccg ctg tcc 1642
Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser
195 200 205

agc ccc aag gtg tgg cgc tgg atc aac gtc gtc gtg gca gtt gtg atg 1690
Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met
210 215 220 225

acc gca ttg gcc atc aaa ctg atg ttg atg ggt tag ttttcgcggg 1736
Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
230 235

ttttggaatc ggtggccttc gcccaaattg tgatgccggc gtcgtgggaa atctcatcga 1796

Seq_listing_US_korrigiert141102.txt

tcgcctccaa ctcggcgctca gaaaactcca agttgttgag tgaatcaagg ctgttgtcca 1856
gctgctcaac tgacgaagca ccaatcaatg cactgggtcac ggtatccgag ccgtactctc 1916
cttgctcgag cagcaccat gcaagcgcca tctgcgcaag tgactgcccg cgttcctggg 1976
cgatgtcatt gagcttgagg accatatcaa tattgttcac gttcaacatg ccctcagaca 2036
gggacttacc ctggctggcg cgggaaccct ctggaattcc atcgagatat ttgtccgtga 2096
gcaggccctg cgcaagtggg gagaaagcaa tgacgccaag accattgttg gcagctgact 2156
gcaacaagtt ctcaccgtca tcgcccgggt cctccacca acgattaatg atggaatagc 2216
ttggctgatg aatcagaagc gggcagccct cctccgcat gaactcagcc gcctccgctg 2276
tgagctctgg accgtaggaa gaaataccca cgtaaagagc cttccagac gcaacaatgt 2336
cacgcaatgc gtacatgggt tcttccaaag gagtatct 2374

<210> 2
<211> 236
<212> PRT
<213> Corynebacterium glutamicum
<220> (LySE)

<400> 2
Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser
1 5 10 15
Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
20 25 30
Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
35 40 45
Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
50 55 60
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
65 70 75 80
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
85 90 95
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
100 105 110
Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn
115 120 125
Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys
130 135 140
Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr
145 150 155 160
Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp
165 170 175

Seq_listing_US_korrigiert141102.txt

Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile
 180 185 190
 Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu
 195 200 205
 Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val
 210 215 220
 Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
 225 230 235

<210> 3
 <211> 2374
 <212> DNA
 <213> Corynebacterium glutamicum
 <220> (complement to <210> 1)
 <221> unsure
 <222> CDS (2)..(652)
 <223> orf3
 <220>
 <221> gene
 <222> CDS (1421)..(2293)
 <223> LysG

<400> 3
 a gat act cct ttg gaa gaa acc atg tac gca ttg cgt gac att gtt gcg 49
 Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala
 1 5 10 15
 tct gga aag gct ctt tac gtg ggt att tct tcc tac ggt cca gag ctc 97
 Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu
 20 25 30
 aca gcg gag gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg 145
 Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu
 35 40 45
 att cat cag cca agc tat tcc atc att aat cgt tgg gtg gag gaa ccg 193
 Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro
 50 55 60
 ggc gat gac ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt 241
 Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu
 65 70 75 80
 ggc gtc att gct ttc tca cca ctt gcg cag ggc ctg ctc acg gac aaa 289
 Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys
 85 90 95
 tat ctc gat gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc 337
 Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser
 100 105 110
 ctg tct gag ggc atg ttg aac gtg aac aat att gat atg gtc cgc aag 385
 Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys
 115 120 125
 ctc aat gac atc gcc cag gaa cgc ggg cag tca ctt gcg cag atg gcg 433

Seq_listing_US_korrigiert141102.txt

Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala
 130 135 140
 ctt gca tgg gtg ctg cgc gag caa gga gag tac ggc gcg gat acc gtg 481
 Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val
 145 150 155 160
 acc agt gca ttg att ggt gct tct tca gtt gag cag ctg gac aac agc 529
 Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser
 165 170 175
 ctt gat tca ctc aac aac ttg gag ttt tct gac gcc gag ttg gag gcg 577
 Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala
 180 185 190
 atc gat gag att tcc cac gac gcc gcc atc aac att tgg gcg aag gcc 625
 Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala
 195 200 205
 acc gat tcc aaa acc cgc gaa aac taa cccatcaaca tcagtttgat 672
 Thr Asp Ser Lys Thr Arg Glu Asn
 210 215
 ggccaatgcg gtcatacaca ctgccacgac gacgttgatc cagcgccaca ccttggggct 732
 ggacagcggg cgtgacaatg ctgctgcgcc gaaaccacc agcggaacc agatcaggct 792
 tgccgcgaac gcgccagcgg cgaaaatcca ccgtccggtg tcgccgtatt gcgcgccgac 852
 gccgccgata aacacaaacg cgtccaaata cgcattcggg ttcaaccagg tcagcacgat 912
 tgccatcaac atgggcttta cccaaacccg ctgcttatcg acgctcacct ccaccgcac 972
 ccggttgcg gtgtcagtgg ccaccgccga accgccc aaa ggcgtgtcat cgggcacggt 1032
 tggttctgtt tcttcaatga tctgtggcgc ttccaccttg tttgtcatgg cgtctttcgc 1092
 tgccatgacg gcaaaccata acaggttaagc gatgccaccc cagcgcataa tatcgagcac 1152
 gatcggcgcg gcattggaca aaagatcaac gcccaagggtg ccggcgatga acaaaaagac 1212
 gtcagaaatt aaacacacga gaagaaccgc aatgagtcct tcgcgcttaa ttccttgttt 1272
 aatcaccagt acattctgcg gtccgatgga cagtaaaaga ctggcccca aaagcagacc 1332
 tgtaatgaag atttccatga tcaccatcgt gacctatgga agtacttaag taaaatgatt 1392
 ggttcttaac atggtttaat atagcttc atg aac ccc att caa ctg gac act 1444
 Met Asn Pro Ile Gln Leu Asp Thr
 220 225
 ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc tcc tta gcc 1492
 Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala Ser Leu Ala
 230 235 240
 ctt tcc att tcc ccc tct gcg gtg agt cag cgc gtt aaa gct ctc gag 1540
 Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys Ala Leu Glu
 245 250 255
 cat cac gtg ggt cga gtg ttg gta tct cgc acc caa ccg gcc aaa gca 1598
 His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro Ala Lys Ala
 260 265 270

Seq_listing_US_korrigiert141102.txt

acc gaa gcg ggt gaa gtc ctt gtg caa gca gcg cgg aaa atg gtg ttg 1636
 Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys Met Val Leu
 275 280 285

ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt gct gaa atc 1684
 Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu Ala Glu Ile
 290 295 300 305

ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca tgg ttt cct 1732
 Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr Trp Phe Pro
 310 315 320

ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg ctc acg ctg 1780
 Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr Leu Thr Leu
 325 330 335

cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg cgt gga gat 1828
 Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg Arg Gly Asp
 340 345 350

gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg gga tgt gaa 1876
 Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala Gly Cys Glu
 355 360 365

gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca acc ccc tca 1924
 Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala Thr Pro Ser
 370 375 380 385

ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg gct gcg atg 1972
 Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp Ala Ala Met
 390 395 400

ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac cgt gac ctg 2020
 Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp Arg Asp Leu
 405 410 415

gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta tcc att gtc 2068
 Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val Ser Ile Val
 420 425 430

ccg tcg gcg gaa ggt ttt ggt gag gca att cgc cga ggc ctt ggt tgg 2116
 Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly Leu Gly Trp
 435 440 445

gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa gca gga gaa 2164
 Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys Ala Gly Glu
 450 455 460 465

gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg tat tgg caa 2212
 Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met Tyr Trp Gln
 470 475 480

cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca gac gcc gtc 2260
 Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr Asp Ala Val
 485 490 495

gtt gat gca gca atc gag gga ttg cgg cct tag ttacttctga aaaggttcag 2313
 Val Asp Ala Ala Ile Glu Gly Leu Arg Pro
 500 505

ggtttttcac ttcttcgccc gcaggaattg ggccaggcag agtaacacct tcagcaaatg 2373

g 2374

Seq_Listing_US_korrigiert141102.txt

<210> 4
 <211> 216
 <212> PRT
 <213> Corynebacterium glutamicum
 <220> (orf3)

<400> 4
 Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala
 1 5 10 15
 Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu
 20 25 30
 Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu
 35 40 45
 Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro
 50 55 60
 Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu
 65 70 75 80
 Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys
 85 90 95
 Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser
 100 105 110
 Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys
 115 120 125
 Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala
 130 135 140
 Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val
 145 150 155 160
 Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser
 165 170 175
 Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala
 180 185 190
 Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala
 195 200 205
 Thr Asp Ser Lys Thr Arg Glu Asn
 210 215

<210> 5
 <211> 290
 <212> PRT
 <213> Corynebacterium glutamicum
 <220> (LysG)

<400> 5
 Met Asn Pro Ile Gln Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly
 1 5 10 15
 Ser Phe Glu Gly Ala Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val

20

25

30

Ser Gln Arg Val Lys Ala Leu Glu His His Val Gly Arg Val Leu Val
 35 40 45
 Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val
 50 55 60
 Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln
 65 70 75 80
 Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala
 85 90 95
 Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser
 100 105 110
 Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr
 115 120 125
 Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu
 130 135 140
 Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg
 145 150 155 160
 His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp
 165 170 175
 Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys
 180 185 190
 Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val
 195 200 205
 Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu
 210 215 220
 Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala
 225 230 235 240
 Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro
 245 250 255
 Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser
 260 265 270
 Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu
 275 280 285
 Arg Pro
 290

FZJ 9910 PCT/US 8/8
 US 09/105,117

12.11.02